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ATGGGTGCGAGAGCGTCAGTATTAAGCGGGGGAGAATTAGATCGATGGGAAAAAAT  
TCGGTTAAGGCCAGGGGGAAAGAAGAAGTACAAGCTAAAGCACATCGTATGGGCAA  
GCAGGGAGCTAGAACGATTCGCAGTTAATCCTGGCCTGTTAGAAACATCAGAAGGC  
TG TAGACAAATACTGGGACAGCTACAACCATCCCTTCAGACAGGATCAGAGGAGCT  
TCGATCACTATACAACACAGTAGCAACCCTCTATTGTGTGCACCAGCGGATCGAGA  
TCAAGGACACCAAGGAAGCTTTAGACAAGATAGAGGAAGAGCAAAACAAGTCCAAG  
AAGAAGGCCCCAGCAGGCAGCAGCTGACACAGGACACAGCAATCAGGTCAGCCAAAA  
TTACCCTATAGTGCAGAACATCCAGGGGGCAAATGGTACATCAGGCCATATCACCTA  
GAACTTTAAATGCATGGGTAAAAGTAGTAGAAGAGAAGGCTTTCAGCCCAGAAGTG  
ATACCCATGTTTTTCAGCATTATCAGAAGGAGCCACCCACAGGACCTGAACACGAT  
GTTGAACACCGTGGGGGGACATCAAGCAGCCATGCAAATGTTAAAAGAGACCATCA  
ATGAGGAAGCTGCAGAATGGGATAGAGTGCATCCAGTGCATGCAGGGCCTATTGCA  
CCAGGCCAGATGAGAGAACCAAGGGGAAGTGACATAGCAGGAAC TACTAGTACCCT  
TCAGGAACAAATAGGATGGATGACAAATAATCCACCTATCCCAGTAGGAGAGATCT  
ACAAGAGGTGGATAATCCTGGGATTGAACAAGATCGTGAGGATGTATAGCCCTACC  
AGCATTCTGGACATAAGACAAGGACCAAGGAACCCTTTAGAGACTATGTAGACCG  
GTTCTATAAACTCTAAGAGCTGAGCAAGCTTCACAGGAGGTAAAAAATTGGATGA  
CAGAAACCTTGTTGGTCCAAAATGCGAACCCAGATTGTAAGACCATCCTGAAGGCT  
CTCGGCCCAGCGGCTACACTAGAAGAAATGATGACAGCATGTCAGGGAGTAGGAGG  
ACCCGGCCATAAGGCAAGAGTTTTGGCCGAGGCGATGAGCCAGGTGACGAAC TCGG  
CGACCATAATGATGCAGAGAGGCAACTTCCGGAACCAGCGGAAGATCGTCAAGTGC  
TTCAATTGTGGCAAAGAAGGGCACACCGCCAGGAAC TGCCGGGGCCCCCGGAAGAA  
GGGCTGTTGGAAATGTGGAAAGGAAGGACACCAAATGAAAGATTGTACTGAGAGAC

FIG. 1A

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AGGCTAATTTTTTAGGGAAGATCTGGCCTTCCTACAAGGGAAGGCCAGGGAATTTT  
CTTCAGAGCAGACCAGAGCCAACAGCCCCACCAGAAGAGAGCTTCAGGTCTGGGGT  
AGAGACAACAACCTCCCCCTCAGAAGCAGGAGCCGATAGACAAGGAACTGTATCCTT  
TAACTTCCCTCAGATCACTCTTTGGCAACGACCCCTCGTCACAGTAAGGATCGGGG  
GGCAACTCAAGGAAGCGCTGCTCGATACAGGAGCAGATGATACAGTATTAGAAGAA  
ATGAGTTTGCCAGGAAGATGGAAACCAAAAATGATAGGGGGGATCGGGGGCTTCAT  
CAAGGTGAGGCAGTACGACCAGATACTCATAGAAATCTGTGGACATAAAGCTATAG  
GTACAGTATTAGTAGGACCTACACCTGTCAACATAATTGGAAGAAATCTGTTGACC  
CAGATCGGCTGCACCTTGAACCTCCCCATCAGCCCTATTGAGACGGTGCCCGTGAA  
GTTGAAGCCGGGGATGGACGGCCCCAAGGTCAAGCAATGGCCATTGACGAAAGAGA  
AGATCAAGGCCTTAGTCGAAATCTGTACAGAGATGGAGAAGGAAGGGAAGATCAGC  
AAGATCGGGCCTGAGAACCCCTACAACACTCCAGTCTTCGCAATCAAGAAGAAGGA  
CAGTACCAAGTGGAGAAAGCTGGTGGACTTCAGAGAGCTGAACAAGAGAACTCAGG  
ACTTCTGGGAAGTTCAGCTGGGCATCCACATCCCGCTGGGTGAAGAAGAAGAAG  
TCAGTGACAGTGCTGGATGTGGGTGATGCCTACTTCTCCGTTCCCTTGGACGAGGA  
CTTCAGGAAGTACACTGCCTTCACGATACCTAGCATCAACAACGAGACACCAGGCA  
TCCGCTACCAGTACAACGTGCTGCCACAGGGATGGAAGGGATCACCAGCCATCTTT  
CAAAGCAGCATGACCAAGATCCTGGAGCCCTTCGCAAGCAAAACCCAGACATCGT  
GATCTATCAGTACATGGACGACCTCTACGTAGGAAGTGACCTGGAGATCGGGCAGC  
ACAGGACCAAGATCGAGGAGCTGAGACAGCATCTGTTGAGGTGGGGACTGACCACA  
CCAGACAAGAAGCACCAGAAGGAACCTCCCTTCCTGTGGATGGGCTACGAACTGCA  
TCCTGACAAGTGGACAGTGCAGCCCATCGTGCTGCCTGAGAAGGACAGCTGGACTG  
TGAACGACATACAGAAGCTCGTGGGCAAGTTGAACTGGGCAAGCCAGATCTACCCA  
GGCATCAAAGTTAGGCAGCTGTGCAAGCTGCTTCGAGGAACCAAGGCACTGACAGA

FIG. IB

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AGTGATCCCCTGACAGAGGAAGCAGAGCTAGAACTGGCAGAGAACCGAGAGATCC  
TGAAGGAGCCAGTACATGGAGTGTACTACGACCCAAGCAAGGACCTGATCGCAGAG  
ATCCAGAAGCAGGGGCAAGGCCAATGGACCTACCAAATCTACCAGGAGCCCTTCAA  
GAACCTGAAGACAGGCAAGTACGCAAGGATGAGGGGTGCCACACCAACGATGTGA  
AGCAGCTGACAGAGGCAGTGCAGAAGATCACCACAGAGAGCATCGTGATCTGGGGC  
AAGACTCCCAAGTTCAAGCTGCCCATAACAGAAGGAGACATGGGAGACATGGTGGAC  
CGAGTACTGGCAAGCCACCTGGATCCCTGAGTGGGAGTTCGTGAACACCCCTCCCT  
TGGTGAAACTGTGGTATCAGCTGGAGAAGGAACCCATCGTGGGAGCAGAGACCTTC  
TACGTGGATGGGGCAGCCAACAGGGAGACCAAGCTGGGCAAGGCAGGCTACGTGAC  
CAACCGAGGACGACAGAAAGTGGTGACCCTGACTGACACCACCAACCAGAAGACTG  
AGCTGCAAGCCATCTACCTAGCTCTGCAAGACAGCGGACTGGAAGTGAACATCGTG  
ACAGACTCACAGTACGCACTGGGCATCATCCAAGCACAACCAGACCAATCCGAGTC  
AGAGCTGGTGAACCAGATCATCGAGCAGCTGATCAAGAAGGAGAAAGTGACCTGG  
CATGGGTACCAGCACACAAAGGAATTGGAGGAAATGAACAAGTAGATAAATTAGTC  
AGTGCTGGGATCCGGAAGGTGCTGTTCCCTGGACGGGATCGATAAGGCCCAAGATGA  
ACATGAGAAGTACCACTCCAACCTGGCGCGCTATGGCCAGCGACTTCAACCTGCCAC  
CTGTAGTAGCAAAGAAATAGTAGCCAGCTGTGATAAATGTCAGCTAAAAGGAGAA  
GCCATGCATGGACAAGTAGACTGTAGTCCAGGAATATGGCAGCTGGACTGCACGCA  
CCTGGAGGGGAAGGTGATCCTGGTAGCAGTTCATGTAGCCAGTGGATATATAGAAG  
CAGAAGTTATCCCTGCTGAAACTGGGCAGGAAACAGCATATTTTCTTTTAAATTA  
GCAGGAAGATGGCCAGTAAAAACAATACACACGGACAACGGAAGCAACTTCACTGG  
TGCTACGGTTAAGGCCGCTGTTGGTGGGCGGGAATCAAGCAGGAATTGGAATTC  
CCTACAATCCCAATCGCAAGGAGTCGTGGAGAGCATGAACAAGGAGCTGAAGAAG  
ATCATCGGACAAGTGAGGGATCAGGCTGAGCACCTGAAGACAGCAGTGCAGATGGC

FIG. 1C

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AGTGTTTCATCCACAACCTTCAAAAGAAAAGGGGGGATTGGGGGGTACAGTGCAGGGG  
AAAGGATCGTGGACATCATCGCCACCGACATCCAAACCAAGGAGCTGCAGAAGCAG  
ATCACCAAGATCCAGAACTTCCGGGTGTACTACCGCGACAGCCGCAACCCACTGTG  
GAAGGGACCAGCAAAGCTCCTCTGGAAGGGAGAGGGGGCAGTGGTGATCCAGGACA  
ACAGTGACATCAAAGTGGTGCCAAGGCGCAAGGCCAAGATCATCCGCGACTATGGA  
AAACAGATGGCAGGTGATGATTGTGTGGCAAGTAGACAGGATGAGGATTAGAACCT  
GGAAGAGCCTGGTGAAGCACCATATG (SEQUENCE ID NO:1)

FIG. ID

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```
>wildtype      TGTACAGAGA TGGAAAAGGA AGGGAAAATT TCAAAAATTG
>mutated      TGTACAGAGA TGGAGAAGGA AGGGAAGATC AGCAAGATCG
#1
.....
          *          * * *** * *

>wildtype      GGCCTGAAAA TCCATACAAT ACTCCAGTAT TTGCCATAAA
>mutated      GGCCTGAGAA CCCCTACAAC ACTCCAGTCT TCGCAATCAA
#41
.....
          * * * * *

>wildtype      GAAAAAAGAC AGTACTAAAT GGAGAAAATT AGTAGATTTC
>mutated      GAAGAAGGAC AGTACCAAGT GGAGAAAGCT GGTGGACTTC
#81
.....
          * * * * *

>wildtype      AGAGAACTTA ATAAGAGAAC TCAAGACTTC TGGGAAGTTC
>mutated      AGAGAGCTGA ACAAGAGAAC TCAGGACTTC TGGGAAGTTC
#121
.....
          * * * *

>wildtype      AATTAGGAAT ACCACATCCC GCAGGGTTAA AAAAGAAAAA
>mutated      AGCTGGGCAT CCCACATCCC GCTGGGTTGA AGAAGAAGAA
#161
.....
          * * * * *

>wildtype      ATCAGTAACA GTACTGGATG TGGGTGATGC ATATTTTTCa
>mutated      GTCAGTGACA GTGCTGGATG TGGGTGATGC CTACTTCTCC
#201
.....
          * * * *

>wildtype      GTTCCCTTAG ATGAAGACTT CAGGAAATAT ACTGCATTTA
>mutated      GTTCCCTTGG ACGAGGACTT CAGGAAGTAC ACTGCCTTCA
#241
.....
          * * * *

>wildtype      CCATACCTAG TATAACAAT GAGACACCAG GGATTAGATA
>mutated      CGATACCTAG CATCAACAAC GAGACACCAG GCATCCGCTA
#281
.....
          * * * *

>wildtype      TCAGTACAAT GTGCTTCCAC AGGGATGGAA AGGATCACCA
>mutated      CCAGTACAAC GTGCTGCCAC AGGGATGGAA GGGATCACCA
#321
.....
          * * *

>wildtype      GCAATATTCC AAAGTAGCAT GACAAAAATC TTAGAGCCTT
>mutated      GCCATCTTTC AAAGCAGCAT GACCAAGATC CTGGAGCCCT
#361
.....
          * * * *

>wildtype      TTAGAAAACA AAATCCAGAC ATAGTTATCT ATCAATACAT
>mutated      TCCGCAAGCA AAACCCAGAC ATCGTGATCT ATCAGTACAT
#401
.....
          * * * * *
          * * * * *
```

FIG. 2A

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```
>wildtype      GGATGATTG TATGTAGGAT CTGACTTAGA AATAGGGCAG
>mutated      GGACGACCTC TACGTAGGAA GTGACCTGGA GATCGGGCAG
#441          .....
              *  **  *  *  *  *  *  *

>wildtype      CATAGAACAA AAATAGAGGA GCTGAGACAA CATCTGTTGA
>mutated      CACAGGACCA AGATCGAGGA GCTGAGACAG CATCTGTTGA
#481          .....
              *  *  *  *  *  *

>wildtype      GGTGGGGACT TACCACACCA GACAAAAAAC ATCAGAAAGA
>mutated      GGTGGGGACT GACCACACCA GACAAGAAGC ACCAGAAGGA
#521          .....
              *  *  *  *

>wildtype      ACCTCCATTC CTTTGGATGG GTTATGAACT CCATCCTGAT
>mutated      ACCTCCCTTC CTGTGGATGG GCTACGAACT GCATCCTGAC
#561          .....
              *  *  *  *  *  *

>wildtype      AAATGGACAG TACAGCCTAT AGTGCTGCCA GAAAAAGACA
>mutated      AAGTGGACAG TGCAGCCCAT CGTGCTGCCT GAGAAGGACA
#601          .....
              *  *  *  *  *  *

>wildtype      GCTGGACTGT CAATGACATA CAGAAGTTAG TGGGGAAATT
>mutated      GCTGGACTGT GAACGACATA CAGAAGCTCG TGGGCAAGTT
#641          .....
              *  *  *  *  *

>wildtype      GAATTGGGCA AGTCAGATTT ACCCAGGGAT TAAAGTAAGG
>mutated      GAACTGGGCA AGCCAGATCT ACCCAGGCAT CAAAGTTAGG
#681          .....
              *  *  *  *  *

>wildtype      CAATTATGTA AACTCCTTAG AGGAACCAAA GCACTAACAG
>mutated      CAGCTGTGCA AGCTGCTTCG AGGAACCAAG GCACTGACAG
#721          .....
              **  *  *  *  *  *

>wildtype      AAGTAATACC ACTAACAGAA GAAGCAGAGC TAGAACTGGC
>mutated      AAGTGATCCC ACTGACAGAG GAAGCAGAGC TAGAACTGGC
#761          .....
              *  *  *  *

>wildtype      AGAAAACAGA GAGATTCTAA AGAACCAGT ACATGGAGTG
>mutated      AGAGAACCGA GAGATCCTGA AGGAGCCAGT ACATGGAGTG
#801          .....
              *  *  *  *  *

>wildtype      TATTATGACC CATCAAAAGA CTTAATAGCA GAAATACAGA
>mutated      TACTACGACC CAAGCAAGGA CCTGATCGCA GAGATCCAGA
#841          .....
              *  *  ***  *  *  *  *
```

FIG. 2B

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```
>wildtype      AGCAGGGGCA AGGCCAATGG ACATATCAA TTTATCAAGA
>mutated      AGCAGGGGCA AGGCCAATGG ACCTACCAA TCTACCAGGA
#881          .....
                * * * * *

>wildtype      GCCATTTAAA AATCTGAAA CAGGAAAATA TGCAAGAATG
>mutated      GCCCTTCAAG AACCTGAAGA CAGGCAAGTA CGCAAGGATG
#921          .....
                * * * * *

>wildtype      AGGGGTGCCC AACTAATGA TGTAACAA TTAACAGAGG
>mutated      AGGGGTGCCC ACACCAACGA TGTGAAGCAG CTGACAGAGG
#961          .....
                * * * * *

>wildtype      CAGTGCAAAA AATAACCACA GAAAGCATAG TAATATGGGG
>mutated      CAGTGCAGAA GATCACCACA GAGAGCATCG TGATCTGGGG
#1001         .....
                * * * * *

>wildtype      AAAGACTCCT AAATTTAAAC TGCCCATACA AAAGGAAACA
>mutated      CAAGACTCCC AAGTTCAAGC TGCCCATACA GAAGGAGACA
#1041         .....
                * * * * *

>wildtype      TGGGAAACAT GGTGGACAGA GTATTGGCAA GCCACCTGGA
>mutated      TGGGAGACAT GGTGGACCGA GTACTGGCAA GCCACCTGGA
#1081         .....
                * * * * *

>wildtype      TTCCTGAGTG GGAGTTTGTT AATACCCCTC CTTTAGTGAA
>mutated      TCCCTGAGTG GGAGTTCGTG AACACCCCTC CCTTGGTGAA
#1121         .....
                * * * * *

>wildtype      ATTATGGTAC CAGTTAGAGA AAGAACCCAT AGTAGGAGCA
>mutated      ACTGTGGTAT CAGCTGGAGA AGGAACCCAT CGTGGGAGCA
#1161         .....
                * * * * *

>wildtype      GAAACCTTCT ATGTAGATGG GGCAGCTAAC AGGGAGACTA
>mutated      GAGACCTTCT ACGTGGATGG GGCAGCCAAC AGGGAGACCA
#1201         .....
                * * * * *

>wildtype      AATTAGGAAA AGCAGGATAT GTTACTAATA GAGGAAGACA
>mutated      AGCTGGGCAA GGCAGGCTAC GTGACCAACC GAGGACGACA
#1241         .....
                * * * * *

>wildtype      AAAAGTTGTC ACCCTAACTG ACACAACAAA TCAGAAGACT
>mutated      GAAAGTGGTG ACCCTGACTG ACACCACCAA CCAGAAGACT
#1281         .....
                * * * * *
```

FIG. 2C

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```
>wildtype      GAGTTACAAG CAATTTATCT AGCTTTGCAG GATTCGGGAT
>mutated       GAGCTGCAAG CCATCTACCT AGCTCTGCAA GACAGCGGAC
#1321          .....
               * * * * *

>wildtype      TAGAAGTAAA CATAGTAACA GACTCACAAT ATGCATTAGG
>mutated       TGGAAAGTGA CATCGTGACA GACTCACAGT ACGCACTGGG
#1361          .....
               * * * * *

>wildtype      AATCATTCAA GCACAACCAG ATCAAAGTGA ATCAGAGTTA
>mutated       CATCATCCAA GCACAACCAG ACCAATCCGA GTCAGAGCTG
#1401          .....
               * * * * *

>wildtype      GTCAATCAAA TAATAGAGCA GTTAATAAAA AAGGAAAAGG
>mutated       GTGAACCAGA TCATCGAGCA GCTGATCAAG AAGGAGAAAG
#1441          .....
               * * * * *

>wildtype      TCTATCTGGC ATGGGTACCA GCACACAAAG GAATTGGAGG
>mutated       TGTACCTGGC ATGGGTACCA GCACACAAAG GAATTGGAGG
#1481          .....
               * *

>wildtype      AAATGAACAA GTAGATAAAT TAGTCAGTGC TGGAAATCAGG
>mutated       AAATGAACAA GTAGATAAAT TAGTCAGTGC TGGGATCCGG
#1521          .....
                           * *

>wildtype      AAAGTACTAT TTTTAGATGG AATAGATAAG GCCCAAGATG
>mutated       AAGGTGCTGT TCCTGGACGG GATCGATAAG GCCCAAGATG
#1561          .....
               * * * * *

>wildtype      AACATGAGAA ATATCACAGT AATTGGAGAG CAATGGCTAG
>mutated       AACATGAGAA GTACCACTCC AACTGGCGCG CTATGGCCAG
#1601          .....
               * * * * *

>wildtype      TGATTTTAAC CTGCCACCTG TAGTAGCAAA AGAAATAGTA
>mutated       CGACTTCAAC CTGCCACCTG TAGTAGCAAA AGAAATAGTA
#1641          .....
               * *

>wildtype      GCCAGCTGTG ATAAATGTCA GCTAAAAGGA GAAGCCATGC
>mutated       GCCAGCTGTG ATAAATGTCA GCTAAAAGGA GAAGCCATGC
#1681          .....

>wildtype      ATGGACAAGT AGACTGTAGT CCAGGAATAT GGCAACTAGA
>mutated       ATGGACAAGT AGACTGTAGT CCAGGAATAT GGCAGCTGGA
#1721          .....
                           * *
```

FIG. 2D



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```
>wildtype      TTGTACACAT TTAGAAGGAA AAGTTATCCT GGTAGCAGTT
>mutated       CTGCACGCAC CTGGAGGGGA AGGTGATCCT GGTAGCAGTT
#1761          .....
               * * * * *

>wildtype      CATGTAGCCA GTGGATATAT AGAAGCAGAA GTTATTCCAG
>mutated       CATGTAGCCA GTGGATATAT AGAAGCAGAA GTTATCCCTG
#1801          .....
               * *

>wildtype      CAGAAACAGG GCAGGAAACA GCATATTTTC TTTTAAATTT
>mutated       CTGAAACTGG GCAGGAAACA GCATATTTTC TTTTAAATTT
#1841          .....
               *

>wildtype      AGCAGGAAGA TGGCCAGTAA AAACAATACA TACAGACAAT
>mutated       AGCAGGAAGA TGGCCAGTAA AAACAATACA CACGGACAAC
#1881          .....
               * * *

>wildtype      GGCAGCAATT TCACCAAGTGC TACGGTTAAG GCCGCCTGTT
>mutated       GGAAGCAACT TCACTGGTGC TACGGTTAAG GCCGCCTGTT
#1921          .....
               * * *

>wildtype      GGTGGGCGGG AATCAAGCAG GAATTGGAA TTCCCTACAA
>mutated       GGTGGGCGGG AATCAAGCAG GAATTGGAA TTCCCTACAA
#1961          .....

>wildtype      TCCCCAAGT CAAGGAGTAG TAGAATCTAT GAATAAAGAA
>mutated       TCCCCAATCG CAAGGAGTCG TGGAGAGCAT GAACAAGGAG
#2001          .....
               * * * * *

>wildtype      TTAAAGAAAA TTATAGGACA GGTAAGAGAT CAGGCTGAAC
>mutated       CTGAAGAAGA TCATCGGACA AGTGAGGGAT CAGGCTGAGC
#2041          .....
               * * * * *

>wildtype      ATCTTAAGAC AGCAGTACAA ATGGCAGTAT TCATCCACAA
>mutated       ACCTGAAGAC AGCAGTGCAG ATGGCAGTGT TCATCCACAA
#2081          .....
               * * * * *

>wildtype      TTTTAAAGA AAAGGGGGGA TTGGGGGGTA CAGTGCAGGG
>mutated       CTTCAAAAGA AAAGGGGGGA TTGGGGGGTA CAGTGCAGGG
#2121          .....
               *

>wildtype      GAAAGAATAG TAGACATAAT AGCAACAGAC ATACAAACTA
>mutated       GAAAGGATCG TGGACATCAT CGCCACCGAC ATCCAAACCA
#2161          .....
               * * * * *
```

FIG. 2E

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```
>wildtype      AAGAATTACA AAAACAAATT ACAAAAATTC AAAATTTTCG
>mutated       AGGAGCTGCA GAAGCAGATC ACCAAGATCC AGAACTTCCG
#2201          .....
               *  *  *  *  *  *  *  *  *  *  *  *

>wildtype      GGTTTATTAC AGGGACAGCA GAAATCCACT TTGGAAAGGA
>mutated       GGTGTACTAC CGCGACAGCC GCAACCCACT GTGGAAGGGA
#2241          .....
               *  *  *  *  *  *  *  *

>wildtype      CCAGCAAAGC TCCTCTGGAA AGGTGAAGGG GCAGTAGTAA
>mutated       CCAGCAAAGC TCCTCTGGAA GGGAGAGGGG GCAGTGGTGA
#2281          .....
               *  *  *  *  *

>wildtype      TACAAGATAA TAGTGACATA AAAGTAGTGC CAAGAAGAAA
>mutated       TCCAGGACAA CAGTGACATC AAAGTGGTGC CAAGGCGCAA
#2321          .....
               *  *  *  *  *  *  *  *

>wildtype      AGCAAAGATC ATTAGGGATT ATGGAAAACA GATGGCAGGT
>mutated       GGCCAAGATC ATCCGCGACT ATGGAAAACA GATGGCAGGT
#2361          .....
               *  *  *  *  *

>wildtype      GATGATTGTG TGGCAAGTAG ACAGGATGAG GATTAGAACA
>mutated       GATGATTGTG TGGCAAGTAG ACAGGATGAG GATTAGAACC
#2401          .....
               *

>wildtype      TGGAAAAGTT TAGTAAAACA CCATATG
>mutated       TGGAAGAGCC TGGTGAAGCA CCATATG
#2441          .....
               *  *  *  *  *
```

FIG. 2F

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```
SIV gag  -----
#1      .....
      ATGGGCGTGAGAACTCCGTCTTGTCAGGGAAGAAAGCAG

SIV gag  -----
#41     .....
      ATGAATTAGAAAAATTAGGCTACGACCCAACGGAAAGAA

SIV gag  -----
#81     .....
      AAAGTACATGTTGAAGCATGTAGTATGGGCAGCAAATGAA

SIV gag  -----
#121    .....
      TTAGATAGATTTGGATTAGCAGAAAGCCTGTTGGAGAACA

SIV gag  -----
#161    .....
      AAGAAGGATGTCAAAAAATACTTTCGGTCTTAGCTCCATT

SIV gag  -----
#201    .....
      AGTGCCAACAGGCTCAGAAAATTTAAAAGCCTTTATAAT

SIV gag  -----
#241    .....
      ACTGTCTGCGTCATCTGGTGCATTACCGCAGAAGAGAAAG

SIV gag  -----
SIVgagDX.. -----
#281    .....
      TGAAACACACTGAGGAAGCAAACAGATAGTGCAGAGACA

SIV gag  -----A--A----T----A--A
SIVgagDX.. -----C--C----C----G--G
#321    .....
      CCTAGTGGTGGAAACAGGAACMACMGAAACYATGCCRAAR

SIV gag  --AAG-A-----
SIVgagDX.. --CTC-C-----
#361    .....
      ACMWSTMGACCAACAGCACCATCTAGCGGCAGAGGAGGAA
```

FIG. 4A

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```
SIV gag      -T-----A--A--A-----T-----
SIVgagDX...-C-----G--G--C-----C-----
#401          .....
          AYTACCCAGTACARCARATMGGTGGTAACTAYGTCCACCT

SIV gag      ----T-AAG-----AT-A--T--C-----A--AT--
SIVgagDX...----C-GTC-----CC-G--C--T-----C--GC--
#441          .....
          GCCAYTRWSCCCGAGAACMYTRAAYGCTGGGTMAARYTG

SIV gag      --A-----A-----A--T-----
SIVgagDX...--C-----G-----G--C-----
#481          .....
          ATMGAGGARAAGAARTTYGGAGCAGAAGTAGTGCCAGGAT

SIV gag      -T-----T-----T-----T-----
SIVgagDX...-C-----C-----C-----C-----
#521          .....
          TYCAGGCACTGTCAGAAGGTTGCACCCCCTAYGACATYAA

SIV gag      T-----T-A--T--T--G-----A-----
SIVgagDX...C-----C-G--C--C--T-----G-----
#561          .....
          YCAGATGYTRAAYTGYGTKGGAGACCATCARGCGGCTATG

SIV gag      -----T---A-A--T--T--A-----
SIVgagDX...-----C---C-T--C--C--C-----
#601          .....
          CAGATYATCMGWGAYATYATMAACGAGGAGGCTGCAGATT

SIV gag      -----
SIVgagDX...-----
#641          .....
          GGGACTTGCAGCACCCACAACCAGCTCCACAACAAGGACA

SIV gag      -----T--T-----A--T
SIVgagDX...-----C--C-----C--C
#681          .....
          ACTTAGGGAGCCGTCAGGATCAGAYATYGCAGGAACMACY

SIV gag      AGT-----A--T-----A-----A--A--A
SIVgagDX...TCC-----T--C-----G-----C--T--G
#721          .....
          WSYTCAGTWGAYGAACARATCCAGTGGATGTACMGWCARC
```

FIG. 4B

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SIV gag -----C--A-----T--A-GA-----  
SIVgagDX..-----G--C-----C--C-TC-----  
#761 .....  
AGAACCCSATMCCAGTAGGCAACATYTACMGKMGATGGAT

SIV gag ---A-----GT----A--A--T--CA-A-----T-----A  
SIVgagDX..---G-----TC----G--G--C--TC-T-----C-----G  
#801 .....  
CCARCTGGGKYTGCARAARTGYGYMGWATGTAYAACCCR

SIV gag --A-----  
SIVgagDX..--C-----  
#841 .....  
ACMAACATTCTAGATGTAAAACAAGGGCCAAAAGAGCCAT

SIV gag -----  
#881 .....  
TTCAGAGCTATGTAGACAGGTCTACAAAAGTTTAAGAGC

SIV gag -----  
#921 .....  
AGAACAGACAGATGCAGCAGTAAAGAATTGGATGACTCAA

SIV gag -----  
#961 .....  
ACACTGCTGATTCAAATGCTAACCAGATTGCAAGCTAG

SIV gag -----  
#1001 .....  
TGCTGAAGGGGCTGGGTGTGAATCCCACCCTAGAAGAAAT

SIV gag -----  
#1041 .....  
GCTGACGGCTTGTC AAGGAGTAGGGGGGCGGGACAGAAG

SIV gag -----  
#1081 .....  
GCTAGATTAATGGCAGAAGCCCTGAAAGAGGCCCTCGCAC

SIV gag -----  
#1121 .....  
CAGTGCCAATCCCTTTTGCAGCAGCCCAACAGAGGGGACC

SIV gag -----  
#1161 .....  
AAGAAAGCCAATTAAGTGTGGAATTGTGGGAAAGAGGGA

FIG. 4C

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```
SIV gag -----  
#1201 .....  
      CACTCTGCAAGGCAATGCAGAGCCCCAAGAAGACAGGGAT  
  
SIV gag -----  
#1241 .....  
      GCTGGAAATGTGGAAAAATGGACCATGTTATGGCCAAATG  
  
SIV gag -----  
#1281 .....  
      CCCAGACAGACAGGCGGGTTTTTTAGGCCTTGGTCCATGG  
  
SIV gag -----  
#1321 .....  
      GGAAAGAAGCCCCGCAATTTCCCCATGGCTCAAGTGCATC  
  
SIV gag -----  
#1361 .....  
      AGGGGCTGATGCCAACTGCTCCCCAGAGGACCCAGCTGT  
  
SIV gag -----  
#1401 .....  
      GGATCTGCTAAAGAACTACATGCAGTTGGGCAAGCAGCAG  
  
SIV gag -----  
#1441 .....  
      AGAGAAAAGCAGAGAGAAAGCAGAGAGAAGCCTTACAAGG  
  
SIV gag -----  
#1481 .....  
      AGGTGACAGAGGATTTGCTGCACCTCAATTCTCTCTTTGG  
  
SIV gag -----  
#1521 .....  
      AGGAGACCAGTAG
```

FIG. 4D

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BsrGI (37)

1 CCTGGCCATTGCATACGTTGTATCCATATCATAATATGTACATTATATTTGGCTCATGTCCAACATTACCGCCATGTTGA  
81 CATTGATTATTGACTAGTTATTAATAGTAATCAATTACGGGGTCATTAGTTTCATAGCCCATATATGGAGTTCCGGGTTAC  
161 ATAACCTACGGTAAATGGCCCGCTGGCTGACCGCCCAACGACCCCGCCCATTTGACGTCAATAATGACGTATGTTCCCA  
241 TAGTAACGCCAATAGGGACTTTCCATTGACGTCAATGGGTGGAGTATTACGGTAAACTGCCACTTGGCAGTACATCAA  
321 GTGTATCATATGCCAAGTACGCCCCCTATTGACGTCAATGACGGTAAATGGCCCGCTGGCATTATGCCAGTACATGAC

SnaBI (432)

401 CTTATGGGACTTTCTACTTGGCAGTACATCTACGTATTAGTCATCGCTATTACCATGGTGATGCGGTTTTGGCAGTACA  
481 TCAATGGGCGTGGATAGCGGTTTGACTCACGGGGATTTCGAAGTCTCCACCCCATTTGACGTCAATGGGAGTTTGTTTTGG  
561 CACCAAAATCAACGGGACTTTCCAAAATGTCGTAACAACTCCGCCCCATTGACGCAAAATGGGCGGTAGGCGGTACGGTG  
641 GGAGGTCTATATAAGCAGAGCTCGTTTAGTGAACCGTCAGATCGCCTGGAGACGCCATCCACGCTGTTTTGACCTCCATA

SacII (746)

721 GAAGACACCGGGACCGATCCAGCCTCCGCGGGCCGCGCTAAGTATGGGATGTCTTGGGAATCAGCTGCTTATCGCCATCT

1▶MetGlyCysLeuGlyAsnGlnLeuLeuIleAlaIleL

801 TGCTTTTAAGTGTCTATGGGATCTATTGTACTCTATATGTCACAGTCTTTTATGGTGTAACAGCTTGGAGGAATGCGACA

13▶euLeuLeuSerValTyrGlyIleTyrCysThrLeuTyrValThrValPheTyrGlyValProAlaTrpArgAsnAlaThr  
881 ATTCCCTCTTTTGTGCAACCAAGAATAGGGATACTTGGGGAACAACTCAGTGCTTACCAGATAATGGTGATTATTGAGA

40▶IleProLeuPheCysAlaThrLysAsnArgAspThrTrpGlyThrThrGlnCysLeuProAspAsnGlyAspTyrSerGly  
961 AGTGGCCCTTAATGTTACAGAAAGCTTTGATGCTGGAATAATACAGTCACAGAACAGGCAATAGAGGATGTATGGCAAC

66▶uValAlaLeuAsnValThrGluSerPheAspAlaTrpAsnAsnThrValThrGluGlnAlaIleGluAspValTrpGlnL  
1041 TCTTTGAGACCTCAATAAAGCCTTGTGTAAAATTATCCCCATTATGCATTACTATGAGATGCAATAAAGTGAGACAGAT

93▶euPheGluThrSerIleLysProCysValLysLeuSerProLeuCysIleThrMetArgCysAsnLysSerGluThrAsp  
1121 AGATGGGGATTGACAAAATCAATAACAACAACAGCATCAACAACATCAACGACAGCATCAGCAAAAGTAGACATGGTCAA

120▶ArgTrpGlyLeuThrLysSerIleThrThrThrAlaSerThrThrSerThrThrAlaSerAlaLysValAspMetValAs  
1201 TGAGACTAGTTCTTGTATAGCCAGGATAATTGCACAGGCTTGAACAAGAGCAAATGATAAGCTGTAAATTCAACATGA

146▶nGluThrSerSerCysIleAlaGlnAspAsnCysThrGlyLeuGluGlnGluGlnMetIleSerCysLysPheAsnMetT

PstI (1329)

1281 CAGGGTTAAAAAGAGACAAGAAAAAGAGTACAATGAACTTGGTACTCTGCAGATTGGTATGTGAACAAGGAATAAC

173▶hrGlyLeuLysArgAspLysLysLysGluTyrAsnGluThrTrpTyrSerAlaAspLeuValCysGluGlnGlyAsnAsn  
1361 ACTGGTAATGAAAGTAGATGTTACATGAACCACTGTAACACTTCTGTTATCCAAGAGTCTTGTGACAAACATTATTGGGA

200▶ThrGlyAsnGluSerArgCysTyrMetAsnHisCysAsnThrSerValIleGlnGluSerCysAspLysHisTyrTrpAs  
1441 TGCTATTAGATTTAGGTATTGTGCACCTCCAGGTTATGCTTTGCTTAGATGTAATGACACAAATTATTCAGGCTTTATGC

226▶pAlaIleArgPheArgTyrCysAlaProProGlyTyrAlaLeuLeuArgCysAsnAspThrAsnTyrSerGlyPheMetP  
1521 CTAAATGTTCTAAGGTGGTGGTCTCTTCATGCACAAGGATGATGGAGACACAGACTTCTACTTGGTTTGGCTTTAATGGA

253▶roLysCysSerLysValValValSerSerCysThrArgMetMetGluThrGlnThrSerThrTrpPheGlyPheAsnGly  
1601 ACTAGAGCAGAAAATAGAACTTATATTTACTGGCATGGTAGGGATAATAGGACTATAATTAGTTTAAATAAGTATTATAA

280▶ThrArgAlaGluAsnArgThrTyrIleTyrTrpHisGlyArgAspAsnArgThrIleIleSerLeuAsnLysTyrTyrAs  
1681 TCTAACAAATGAAATGTAGAAGACCAGGAATAAGACAGTTTTACCAGTCACCATTATGCTGGATTGGTTTTCCACTCAC

306▶nLeuThrMetLysCysArgArgProGlyAsnLysThrValLeuProValThrIleMetSerGlyLeuValPheHisSerG

XcmI (1778)

1761 AACCAATCAATGATAGGCCAAAGCAGGCATGGTGTGGTTTGGAGGAAATGGAAGGATGCAATAAAAGAGGTGAAGCAG

333▶InProIleAsnAspArgProLysGlnAlaTrpCysTrpPheGlyGlyLysTrpLysAspAlaIleLysGluValLysGln  
1841 ACCATTGTCAAACATCCAGGTATACTGGAACATAACAATACTGATAAAATCAATTTGACGGCTCCTGGAGGAGGAGATCC

360▶ThrIleValLysHisProArgTyrThrGlyThrAsnAsnThrAspLysIleAsnLeuThrAlaProGlyGlyGlyAspPr  
1921 GGAAGTTACCTTCATGTGGACAAATTGCAGAGGAGAGTTCTCTACTGTAAAAATGAATTGGTTTCTAAATTGGGTAGAAG

386▶oGluValThrPheMetTrpThrAsnCysArgGlyGluPheLeuTyrCysLysMetAsnTrpPheLeuAsnTrpValGluA  
2001 ATAGGAATACAGCTAACCAAGCCAAAGGAACAGCATAAAGGAATTACGTGCCATGTCATATTAGACAAATAATCAAC

413▶spArgAsnThrAlaAsnGlnLysProLysGluGlnHisLysArgAsnTyrValProCysHisIleArgGlnIleIleAsn

FIG. 17A

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PmlI (2134)  
2081 ACTTGGCATAAAGTAGGCCAAAAATGTTTATTTGCCTCCAAGAGAGGGAGACCTCACGTGTAACCTCCACAGTGACCACTCT  
440 Thr TrpHisLysValGlyLysAsnValTyrLeuProProArgGluGlyAspLeuThrCysAsnSerThrValThrSerLe  
2161 CATAGCAAACATAGATTGGATTGATGGAAACCAACTAATATCACCATGAGTGCAGAGGTGCCAGAACTGTATCGATTGG  
466 uIleAlaAsnIleAspTrpIleAspGlyAsnGlnThrAsnIleThrMetSerAlaGluValAlaGluLeuTyrArgLeuG  
2241 AATTGGGAGATTATAAATTAGTAGAGATCACTCCAATTGGCTTGGCCCCACAGATGTGAAGAGGTACACTACTGGTGGC  
493 IuLeuGlyAspTyrLysLeuValGluIleThrProIleGlyLeuAlaProThrAspValLysArgTyrThrThrGlyGly  
BspMI (2378)  
2321 ACCTCAAGAAATAAAAGAGGGGTCTTTGTGCTAGGGTTCTTGGGTTTTCTCGCAACGGCAGGTTCTGCAATGGGAGCCGC  
520 ThrSerArgAsnLysArgGlyValPheValLeuGlyPheLeuGlyPheLeuAlaThrAlaGlySerAlaMetGlyAlaAl  
2401 CAGCCTGACCTCACGGCACAGTCCCGAAGTTTATTGGCTGGGATAGTCCAACAGCAGCAACAGCTGTTGGACGTGGTCA  
546 aSerLeuThrLeuThrAlaGlnSerArgThrLeuLeuAlaGlyIleValGlnGlnGlnGlnGlnLeuLeuAspValValL  
Eam1105I (2502)  
2481 AGAGACAACAAGAATTGTTGCGACTGACCGTCTGGGGAACAAAGAACCTCCAGACTAGGGTCACTGCCATCGAGAAGTAC  
573 ysArgGlnGlnGluLeuLeuArgLeuThrValTrpGlyThrLysAsnLeuGlnThrArgValThrAlaIleGluLysTyr  
2561 TTAAAGGACCAGGCGCAGCTGAATGCTTGGGGATGTGCGTTTAGACAAGCTGCCACACTACTGTACCATGGCCAAATGC  
600 LeuLysAspGlnAlaGlnLeuAsnAlaTrpGlyCysAlaPheArgGlnValCysHisThrThrValProTrpProAsnAl  
2641 AAGTCTAACACCAAAGTGAACAATGAGACTTGGCAAGAGTGGGAGCGAAAGGTTGACTTCTTGAAGAAAATATAACAG  
626 aSerLeuThrProLysTrpAsnAsnGluThrTrpGlnGluTrpGluArgLysValAspPheLeuGluGluAsnIleThrA  
2721 CCTCTAGAGAGGCACAAATTCAACAAGAGAAGAATGTATGAATTACAAAGTTGAATAGCTGGGATGTGTTGGC  
653 IuLeuLeuGluGluAlaGlnIleGlnGlnGluLysAsnMetTyrGluLeuGlnLysLeuAsnSerTrpAspValPheGly  
2801 AATTGGTTTGACCTTGCTTCTTGGATAAAGTATATACAATATGGAGTTTATATAGTTGTAGGAGTAATACTGTTAAGAAT  
680 AsnTrpPheAspLeuAlaSerTrpIleLysTyrIleGlnTyrGlyValTyrIleValValGlyValIleLeuLeuArgIle  
2881 AGTGATCTATATAGTACAAATGCTAGCTAAGTTAAGGCAGGGGTATAGGCCAGTGTTCTCTTCCCCACCTCTTATTTC  
706 eValIleTyrIleValGlnMetLeuAlaLysLeuArgGlnGlyTyrArgProValPheSerSerProProSerTyrPheG  
PpuMI (2979)  
2961 AGCAGACCCATATCCAACAGGACCGGCCTGCCAACAGAGAAGGCAAAGAAAGAGACGGTGGAGAAGCGCGTGGCAAC  
733 IlnGlnThrHisIleGlnGlnAspProAlaLeuProThrArgGluGlyLysGluArgAspGlyGlyGluGlyGlyAsn  
3041 AGCTCTCGCCTTGGCAGATAGAAATATATCCACTTTCTTATTCGTACAGCTTATTAGACTCTTGACTTGGCTATTACGTAA  
760 SerSerTrpProTrpGlnIleGluTyrIleHisPheLeuIleArgGlnLeuIleArgLeuLeuThrTrpLeuPheSerAs  
3121 CTGTAGGACTTTGCTATCGAGAGTATACCAGATCCTCCAACCAATACTCCAGAGGCTCTCTGGCACCTACAGAGGATTC  
786 nCysArgThrLeuLeuSerArgValTyrGlnIleLeuGlnProIleLeuGlnArgLeuSerAlaThrLeuGlnArgIleA  
Bsu36I (3208)  
3201 GAGAAGTCTCAGGACTGAAGTACCTACCTACAATATGGGTGGAGCTATTTCATGAGGCGGTCCAGGCCGTCTGGAGA  
813 rgGluValLeuArgThrGluLeuThrTyrLeuGlnTyrGlyTrpSerTyrPheHisGluAlaValGlnAlaValTrpArg  
3281 TCTGCGACAGAGACTCTTGGGGGCGGTGGGGAGACTTATGGGAGACTCTTAGGAGAGGTGGAAGATGGATACTCGCAAT  
840 SerAlaThrGluThrLeuAlaGlyAlaTrpGlyAspLeuTrpGluThrLeuArgArgGlyGlyArgTrpIleLeuAlaIle  
BamHI (3418)  
EcoRI (3412)  
3361 CCCCAGGAGGATTAGACAAGGGCTTGAGCTCACTCTCTGTGAGGGACAGAGAATTCGGATCCtaggttctagaCTCGA  
866 eProArgArgIleArgGlnGlyLeuGluLeuThrLeuLeu...  
Eco47III (3457)  
3441 GGGGGGGCCCGGTACGAGCGCTTAGCTAGCTAGAGACCCTCCCTGCGAGCTAAGCTGGACAGCCAATGACGGGTAA  
3521 AGAGTGACATTTTCTACTAACCTAAGACAGGAGGGCCGTCAGAGCTACTGCCTAATCCAAAGACGGGTAAAAGTGATAAA  
BstEII (3673)  
3601 AATGTATCACTCCAACCTAAGACAGGCGCAGCTCCGAGGGATTGTGCTGCTGTTTTATATATATTTAAAGGGTGACCT

FIG. 17B



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BsaBI (3740)  
3681 GTCCGGAGCCGTGCTGCCCGGATGATGTCTTGGTCTAGACTCGAGGGGGGGCCCGGTACGATCCAGATCTGCTGTGCCTT  
3761 CTAGTTGCCAGCCATCTGTTGTTTGGCCCTCCCGTGCCTTCCTTGACCTGGAAGGTGCCACTCCCCTGTCTTCC  
3841 TAATAAAATGAGGAAATTCATCGCATTGTCTGAGTAGGTGTCATTCTATTCTGGGGGTGGGTGGGGCAGCACAGCAA

SphI (3948) KpnI (3976)  
3921 GGGGGAGGATTGGGAAGACAATAGCAGGATGCTGGGATGCGGTGGGCTCTATGGGTACCCAGGTGCTGAAGAATTGAC

BstXI (4060)  
4001 CCGGTTCTCTGGGCCAGAAAGAAGCAGGCACATCCCCTTCTCTGTGACACACCCTGTCCACGCCCTGGTTCTTAGTT  
4081 CCAGCCCCACTCATAGGACACTCATAGCTCAGGAGGGCTCCGCCTTCAATCCACCCGCTAAAGTACTTGGAGCGGTCTC  
4161 TCCCTCCCTCATCAGCCCAACAAACCTAGCCTCCAAGAGTGGGAAGAAATTAAAGCAAGATAGGCTATTAAGTGC

XmnI (4293)  
4241 AGAGGGAGAGAAATGCCTCCAACATGTGAGGAAGTAATGAGAGAAATCATAGAATTTCTTCGGCTTCTCGCTCACTGA

StuI (5368)  
4321 CTCGCTGCGCTCGGTGCTTCGGCTGCGGCGAGCGGTATCAGCTCAACAGCGGTAATACGGTTATCCACAGAATCAG  
4401 GGGATAACGCAGGAAAGAACATGTGAGCAAAAGGCCAGCAAAAGGCCAGGAACCGTAAAAAGGCCGGTGTCTGGCGTTT  
4481 TTCCATAGGCTCCGCCCTGACGAGCATCAAAAAATCGAGCTCAAGTCAGAGGTGGCGAAACCCGACAGGACTATA  
4561 AAGATAACAGGCGTTTCCCCCTGGAAGCTCCCTCGTGCGCTCTCTGTTCCGACCCCTGCCGCTTACCGGATACCTGTCCG  
4641 CCTTCTCCCTTCGGGAAGCGTGGCGCTTCTCAATGCTCAOGCTAGGTATCTCAGTTCGGTGTAGGTGCTTCGCTCC  
4721 AAGCTGGGCTGTGTGCAGAACCCCGCTTCAGCCCGACCGCTGCGCTTATCCGGTAACTATCGTCTTAGTCCAACCC  
4801 GGTAAAGACAGCACTTATCGCCACTGGCAGCAGCCACTGGTAACAGGATTAGCAGAGCGAGGTATGTAGGCGGTGCTACAG  
4881 AGTCTTGAAGTGGTGGCCTAACTACGGCTACACTAGAAGGACAGTATTGGTATCTGCGCTCTGCTGAAGCCAGTTACC  
4961 TTCGAAAAAGAGTTGGTAGCTCTTGATCCGGCAACAAACCCGCTGGTAGCGGTGGTTTTTTTGTGTTGCAAGCAGCA  
5041 GATTACGGCGCAGAAAAAAGGATCTCAAGAAGATCCTTTGATCTTTTCTACGGGCTGACGCTCAGTGAACGAAAACT  
5121 CACGTTAAGGATTTTGGTCATGAGATTATCAAAAAGGATCTTCACTAGATCCTTTTAAATTAAAAATGAAGTTTAAA  
5201 TCAATCTAAAGTATATATGAGTAACTTGGTCTGACAGTTACCAATGCTTAATCAGTGAGGCACCTATCTCAGCGATCTG  
5281 TCTATTTCGTTTCATCCATAGTTGCCTGACTCCGGGGGGGGGGCGCTGAGGTCTGCCTCGTGAAGAAGGTGTTGCTGAC

PvuI (5993)  
5361 TCATACCAGGCCTGAATCGCCCCATCATCCAGCCAGAAAGTGAGGGAGCCACGGTTGATGAGAGCTTTGTTGTAGGTGGA  
5441 CCAGTTGGTGATTTTGAACTTTGTCTTTGCCACGGAAACGGTCTGCGTTGTGCGGAAGATGCGTGATCTGATCCTTCACT  
5521 CAGCAAAAGTTCGATTATTCAACAAAGCCCGCTCCCGCTCAAGTCAGCGTAATGCTCTGCGGATTTACAACCAATTA  
5601 CCAATTCTGATTAGAAAACTCATCGAGCATCAATGAAACTGCAATTTATTTCATATCAGGATTATCAATACCATATTTT

SgfI (5992)  
5681 TGAAAAAGCGTTTCTGTAATGAAGGAGAAAACTCACCGAGGCAGTTCCATAGGATGGCAAGATCCTGGTATCGGTCTGC  
248 InPheLeuArgLysGlnLeuSerProSerPheGluGlyLeuCysAsnTrpLeuIleAlaLeuAspGlnTyrArgAspAla  
5761 GATTCGAGCTCGTCCAACATCAATAACCTATTATTTCCCTCGTCAAAAATAAGGTTATCAAGTGAGAAATCACCAT  
222 IleGlyValAlaArgGlyValAspIleCysGlyIleLeuLysGlyGluAspPheIleLeuAsnAspLeuSerPheAspGlyYH  
5841 GAGTGACGACTGAATCCGGTGAGAATGGCAAAAGCTTATGCATTTCTTCCAGACTTGTTCACAGGCCAGCCATTACGC  
195 sThrValValSerAspProSerPheProLeuLeuLysHisMetGluLysTrpValGlnGluValProTrpGlyAsnArgG

BsrFI (6036) SspI (6067)  
5921 TCGTCATCAAAATCACTCGCATCAACCAACCGTTATTTCATTCGTGATTGCGCTGAGCGAGACGAAATACGGATCGCT  
168 LuAspAspPheAspSerAlaAspValLeuGlyAsnAsnMetArgSerGlnAlaGlnAlaLeuArgPheValArgAspSer

SmaI (6118)  
6001 GTTAAAGGACAATTACAAACAGGAATCGAATGCAACCGCGCAGGAACACTGCCAGCGCATCAACAATATTTTCACCTG  
142 AsnPheProCysAsnCysValProIleSerHisLeuArgArgLeuPheValAlaLeuAlaAspValIleAsnGluGlySe

NruI (6335)  
6081 AATCAGGATATTCTTCTAATACCTGGAATGCTGTTTTCCCGGGGATCGCAGTGGTGAGTAACCATGCATCATCAGGAGTA  
115 rAspProTyrGluGluLeuValGlnPheAlaThrLysGlyProIleAlaThrThrLeuLeuTrpAlaAspAspProThrA  
6161 CGGATAAAATGCTTGATGGTCCGAAGAGGCATAAATCCGTCAGCCAGTTAGTCTGACCATCTCATCTGTAACATCATT  
88 rGllePheHisLysIleThrProLeuProMetPheGluThrLeuTrpAsnLeuArgValMetGluAspThrValAspAsn  
6241 GGCAACGCTACCTTTGCCATGTTTCAGAAACAACCTCGCGCATCGGGCTTCCCATACAATCATAGATTGTCGCACCTG  
62 AlaValSerGlyLysGlyHisLysLeuPheLeuGluProAlaAspProLysGlyTyrLeuArgTyrIleThrAlaGlySe

DrallI (6523)  
6321 ATTGCCCGACATTATCGCGAGCCCATTTATACCCATATAAATCAGCATCCATGTTGGAATTTAATCGCGGCCCTCGAGCAA  
35 rGlnGlyValAsnAspArgAlaTrpLysTyrGlyTyrLeuAspAlaAspMetAsnSerAsnLeuArgProArgSerCysS  
6401 GACGTTTCCCGTTGAATATGGCTCATAACCCCCTTGATTACTGTTTATGTAAGCAGACAGTTTATTGTTTCATGATGA  
84 erThrGluArgGlnIleHisSerMet

FIG. 17C

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6641 TTCCCCGAAAAGTGCCACCTGACGTCTAAGAAACCATTATTATCATGACATTAACTATAAAAAATAGGCGTATCACGAG  
6721 GCCCTTTCGTCTCGCGCGTTTCGGTGATGACGGTGAAAACCTCTGACACATGCAGCTCCCGGAGACGGTCACAGCTTGTC  
6801 TGTAAGCGGATGCCGGGAGCAGACAAGCCCGTCAGGGCGGTGAGCGGGTGTGGCGGGTGTGGGGCTGGCTTAACAT  
6881 GCGGCATCAGAGCAGATTGTACTGAGAGTGCACCATATGCGGTGTGAAATACCGCACAGATGCGTAAGGAGAAAATACCG  
6961 CATCAGATTGGCTATTGG

FIG. 17D